

Docket No. CL001181DIV2
 Serial No. To Be Assigned
 Inventors: Ming-Hui WEI et al.
 Title: ISOLATED HUMAN ENZYME PROTEINS...

1 TGGAGGAGCC AGCGGAAGGA CGGTGTGCGG GCGGGCCAGC CCTGGACGAA
 51 AGAAGAGGGC CCCTCCAGGC CAGTCTGGC ACCCTGGAT AGCGGCTGCA
 101 GCCAGGCATG GCGACTCTG CACAGGCCA GAAGCTGGTG TACCTGGTCA
 151 CAGGGGGCTG TGGCTTCTG GGAGAGCACG TGGTGCAGAT GCTGCTGCA
 201 CGGGAGCCCC GGCTCGGGGA GCTGCGGTC TTTGACCAAC ACCTGGGTCC
 251 CTGGCTGGAG GAGCTGAAGA CAGGTACCCG GAACGTGATC GAGGCTTGTG
 301 TGCAGACCGG AACACGGTTC CTGGTCTACA CCAGCAGCAT GGAAGTTGTG
 351 GGGCTAACCA CCAAAGGTCA CCCCTCTAC AGGGGCAACG AAGACACCCC
 401 ATACGAAGCA GTGCACAGGC ACCCCCTATCC TTGCAGCAAG GCCCTGGCCG
 451 AGTGGCTGGT CCTGGAGGCC AACGGGAGGA AGGTCCGTGG GGGGCTGCCC
 501 CTGGTGACGT GTGCCCTTCG TCCCACGGC ATCTACGGTG AAGGCCACCA
 551 GATCATGAGG GACTTCTACC GCCAGGGCCT GCGCCTGGGA GGTTGGCTCT
 601 TCCGGCCAT CCCGGCCTCT GTGGAGCATG GCGGGTCTA TGTGGGCAAT
 651 GTTGCCTGGA TGCACGTGCT GGCAGCCCG GAGCTGGAGC AGCGGGCAGC
 701 CCTGATGGGC GGCCAGGTAT ACTTCTGCTA CGATGGATCA CCCTACAGGA
 751 GCTACGAGGA TTCAACATG GAGTTCTGG GCGCCCTGCGG ACTGCGGCTG
 801 GTGGCGCCC GCCCATTGCT GCCCTACTGG CTGCTGGTGT TCCCTGGCTG
 851 CCTCAATGCC CTGCTGCGT GGCTGCTGCG GCACTGGTG CTCTACGCA
 901 CCCCTGCTGAA CCCCTACACCG CTGGCCGTGG CCAACACCCAC CTTCACCGTC
 951 AGCACCGAACAGGCTCAGCG CCATTTCTGG TATGAGGCCCC TGTTCTCGT
 1001 GGAGGATAGC CGGACCCCGA CCATTCTCTG GGTACAGGCC GCTACGGGTT
 1051 CAGCCCAGTG ACGGTGGGGC TGGGGCTCTGG AGGGCCAGAT ACAGCACATC
 1101 CACCCAGGTC CCGAGCCCTC ACACCCCTGGA CGGGAAGGGA CAGCTGCATT
 1151 CCAGCAGCAG AGGCAGGGCT CTGGGGCCAG AATGGCTGTC CTTGTCGTAG
 1201 AGCCCTCCAC ATTTTCTTT TCTTTTTTGA GACAGGGTCT TGCTCTGTC
 1251 CCCAGACTGG AGTGCAGTGG TGTGATCATA GCTCACTGCA CCCTCAACCT
 1301 CCTGGGTTCA AGCAATCCTC CTGCCCTCAGC CTCTGAACA GCTGGGACCA
 1351 CAGGTGCACG CCACCATACCG TGGCTTTTTT TTGTTGCTTT TAGAGACAGG
 1401 GTCTCACTAT ATTGCTCAAG GCTGGACTTG AACTCCCTGG CTCAAGTGT
 1451 CTTCCCACGT GGGCCTCCCA AAACGCTGGA ACTACAAGTG TGAGGCCACCG
 1501 CGCCTGGCCC ACCGCCTCTC CACATTTCA ATCCAGGAGC CTTGAGTCTG
 1551 TGGCTGTGTC CTGACACCTC CAGAGTTCTG AGGGCCGTCA GGACACGGGA
 1601 GGGTTTGGGG ACAGAGTGTG CTTCCCTCTG CCTATCATCA CCAGTCCTGA
 1651 TGGCCGTTG GTGAGTGTCT GGTGCCCTGG TGGCTTGCCTC CAGCTCTCTT
 1701 GTGGCTTTCT GAGCAGGAAG CGAGCACTAG GCTCCACAGG CTTACGCTGT
 1751 GTCTCCTGCC AGCCACACAG CGACCCATCG GTGCAGAGTG CAGACGCGGG
 1801 TGTGGTTCCCT CGAGCCCACTC TCAGTCCCTC TTTGGGAGGT GATGTTCCA
 1851 TTGTTTTCTA AAGGCCCTCAC CTTCAACTGT TCTGTTTTAG AATTCCCCCTC
 1901 TGGAGGGCTA TGGCCTCCCT ATGGTTTCAC TTCCACCTA CTTCTACCTA
 1951 AGTTCCCTTCC CAGCACATCG CCAGCCCTGG GCCTGGGAT GTCCCCAATG
 2001 CTGTACCTGG CTGACCCCGG ATTAAAAGCC TCATCCACGA AAAAAAAA
 2051 AAAAAAAAAA AAAAAAAAAA A

(SEQ ID NO: 1)

FEATURES:

5'UTR: 1-107
 Start Codon: 108
 Stop Codon: 1059
 3'UTR: 1062

HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

CRA 335001098696094 /altid=gi 11545403 /def=gb AAG37824.1 AF277...	638	0.0
CRA 335001098696092 /altid=gi 11545401 /def=gb AAG37823.1 AF277...	562	e-159
CRA 18000005106837 /altid=gi 2563999 /def=dbj BAA22931.1 (AB00...	484	e-136
CRA 18000005043125 /altid=gi 9629084 /def=ref NP_044103.1 MC15...	269	3e-71
CRA 89000000192042 /altid=gi 9634716 /def=ref NP_039008.1 ORF ...	257	2e-67
CRA 18000004899504 /altid=gi 540666 /def=pir S41971 3beta-hydri...	240	1e-62
CRA 335001098644340 /altid=gi 11251676 /def=pir T37430 hydrox...	213	2e-54
CRA 18000004942649 /altid=gi 112779 /def=sp P26670 3BHS_VACCV 3...	212	4e-54

FIGURE 1A

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CRA|18000004942648 /altid=gi|9791111 /def=ref|NP_063838.1| A44L... 211 9e-54
CRA|73000005493670 /altid=gi|9634564 /def=ref|NP_038102.1| TA55... 211 9e-54

FIGURE 1B

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EST:

gi 11283574 /dataset=dbest /taxon=96...	1283	0.0
gi 11643588 /dataset=dbest /taxon=96...	1116	0.0
gi 13134586 /dataset=dbest /taxon=960...	527	e-147
gi 9334685 /dataset=dbest /taxon=960...	462	e-128

EXPRESSION INFORMATION FOR MODULATORY USE:

gi 11283574	brain
gi 11643588	kidney
gi 13134586	colon
gi 9334685	uterus

FIGURE 1C

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1 MADSAQAQKL VYLVTVGGCGF LGEHVVRMILL QREPRLGELR VFDQHLPWL
51 EELKTGTRNV IEACVQTGTR FLVYTSSMEV VGPNTKGHPF YRGNEDTPYE
101 AVHRHPYPCS KALAEWLVLIE ANGRKVRGGL PLVTCALRPT GIYGEGHQIM
151 RDFYRQGLRL GGWLFRAlPA SVEHGRVYVG NVAWMHVLAA RELEQRAALM
201 GGQVYFCYDG SPYRSYEDFN MEFLGPCGLR LVGARPLLPY WLLVFLAALN
251 ALLQWLLRPL VLYAPLLNPY TLAVANTTFT VSTDKAQRHF GYEPLFSWED
301 SRTRTILWVQ AATGSAQ

(SEQ ID NO: 2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

276-279 NTTF

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

283-285 TDK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 4

1 76-79 SSME
2 97-100 TPYE
3 215-218 SYED
4 297-300 SWED

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

92-99 RGNEDTPY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

157-162 GLRLGG

[6] PDOC00009 PS00009 AMIDATION
Amidation site

122-125 NGRK

[7] PDOC00029 PS00029 LEUCINE_ZIPPER
Leucine zipper pattern

246-267 LAALNALLQWLLRPLVLYAPLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	6	26	0.633	Putative
2	237	257	1.571	Certain
3	260	280	0.819	Putative

FIGURE 2A

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BLAST Alignment to Top Hit:

>CRA|335001098696094 /altid=gi|11545403
 /def=gb|AAG37824.1|AF277719_1 (AF277719) 3
 beta-hydroxy-delta 5-C27-steroid oxidoreductase [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
 /length=369
 Length = 369

Score = 638 bits (1627), Expect = 0.0
 Identities = 315/369 (85%), Positives = 316/369 (85%), Gaps = 52/369 (14%)

Query: 1 MADSAQAQKLVLYVTGGCGFLGEHVRMILLQREPRLGELRVFDQHLPWLEELKTG---- 56
 MADSAQAQKLVLYVTGGCGFLGEHVRMILLQREPRLGELRVFDQHLPWLEELKTG

Sbjct: 1 MADSAQAQKLVLYVTGGCGFLGEHVRMILLQREPRLGELRVFDQHLPWLEELKTGPVRV 60

Query: 57 -----TRNVIEACVQTG 68
 TRNVIEACVQTG

Sbjct: 61 TAIQGDVTQAHEVAAVAGAHVVIHTAGLVDVFGRASPKTIHEVNQGTRNVIEACVQTG 120

Query: 69 TRFLVYTSSMEVVGPNKGHPFYRGNEDETPYEAVHRHPYPCSKALAELWVLEANGRKVRG 128
 TRFLVYTSSMEVVGPNKGHPFYRGNEDETPYEAVHRHPYPCSKALAELWVLEANGRKVRG

Sbjct: 121 TRFLVYTSSMEVVGPNKGHPFYRGNEDETPYEAVHRHPYPCSKALAELWVLEANGRKVRG 180

Query: 129 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAPASVEHGRVYVGNVAVMHVL 188
 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAPASVEHGRVYVGNVAVMHVL

Sbjct: 181 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAPASVEHGRVYVGNVAVMHVL 240

Query: 189 AARELEQRAALMGGQVYFCYDGSPYRSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA 248
 AARELEQRAALMGGQVYFCYDGSP+RSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA

Sbjct: 241 AARELEQRAALMGGQVYFCYDGSPHRSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA 300

Query: 249 LNALLQWLLRPLVLVYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 308
 LNALLQWLLRPLVLVYAPLLNPYTLAVAN TFTVSTDKAQRHFGYEPLFSWEDSRTRTILW

Sbjct: 301 LNALLQWLLRPLVLVYAPLLNPYTLAVANATFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 360

Query: 309 VQAATGSAQ 317

VQAATGSAQ

Sbjct: 361 VQAATGSAQ 369 (SEQ ID NO: 4)

Hmmr search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF01073	3-beta hydroxysteroid dehydrogenase/isomeras	558.2	5.5e-164	2
PF01370	NAD dependent epimerase/dehydratase family	13.3	0.005	1
PF00438	S-adenosylmethionine synthetase	1.8	0.78	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01370	1/1	12	31	..	1	20	[.] 13.3 0.005
PF01073	1/2	1	52	[.]	1	53	[.] 69.6 3.9e-18
PF00438	1/1	289	299	..	365	376	[.] 1.8 0.78
PF01073	2/2	55	313	..	159	425	[.] 489.6 2.4e-143

FIGURE 2B

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1 ATTTGCATTA GCGGGTGGCA GCCAACAGGT GCCTGTTTG GAGAGAGGTC
51 CAGGGAGGAG AGATGAGCAG GGTGCCGTTG GTGACATGGC CAGTCATTTC
101 AGGAGCTGCC CCAACCCAG ACTGCCCA GCAGTCCGGG ACCCCACTGT
151 GACCAGGCAAG ATGCTGAAG GAGTCAGTGG CTCTCTTAC CAGTCAGAT
201 TTCCCTGGAG TTCCCTGCGG GTGACTTAGA ATGGCCACCA GAGGCTTAGG
251 ATGCTGCCCA AAAGAGGGAG GGCTCCTGGA AGCAGAGTCG AGAGAGTCAG
301 TGCCGGGTTA GCGGGAGCTG GAGGCAGAGC TGCAAGCTCCA GGCCTGGTGG
351 GCGTGGACCT GGGGTGCTGG CTGGCAGGCG TGCTCAGGGG CAGGAAGTGG
401 GGGACTCTTC CCTGACCATC GCATCTCACC CTGGCAGATG GTGGCCGACA
451 TGCGGGAGAA GCGCTACGTG CAGGAGGGCA TTGGCAGCAG CTACCTGTT
501 CGGGTGGACC ACGACACCAT CATCGATGCC ACCAAGTGTG GCAACCTGGC
551 CAGATTCACT AACCACTGCT GCACGGTGCG CCAGGGGCA GCGGGGCG
601 GAGTTGGGGG TCGGTGGGGG TGGCCACGGC TCACACGCC TTCCATCCGC
651 AGCCTAAGTCTG CTACGCCAAG GTCATCACCA TCGAGTCCC GAAGAAGATC
701 GTGATCTACT CCAAGCAGCC CATTGGCGTG GACGAGGAGA TCACCTACGA
751 CTACAAGTTC CCACTGGAAG ACAACAAGAT CCCGTGTCTG TGTGGCACAG
801 AGAGCTGCCG GGGCTCCCTA AACTGAGGTG GGGCAGGATG GGTGCCAC
851 CCCCTATTAA TTCCCCCTGG TGCCCTGAGC TCCCAGCACC CCCCCAGCCT
901 TAGTGGGCTC AGCAGGGCCC ACATGCCCACTCCTCAAGC GTGGGGTTGG
951 GGGCCCAAG CCCAGCGAGG GAGCCTCAGT CCCCTGGACGC AGCTTCTG
1001 TCTCCTGTCG CCCCTGCCCA CCACCCCCCTG ATTGTTTTTC TTTGGGAGA
1051 AGAAGCTGTA AATGTTTTG AGCAGGCCAGC AGCTGTTTCC TGTGGAAACC
1101 TGGGGTGGCG GCCTGTACAG ATTCTGTCCT GGGGGGCTAC ACAGTCTCT
1151 CGCTTGTGT TAATGGGAC TTCCCCCTAC GCCCTGGCTG TACCCCTC
1201 CAGTTAGGG GTCTCTGGGG CAGTGGCCAT GTTCTCCCCC TGGGGGGCT
1251 CTGCACCCCCC AGTCCTGGGG ACTCCGTGCC TGAAACCTG CCTCATCTGT
1301 TCCTGCCAGA CCCTGAGGGT CACCCCTCCA CCCTGGTGTC ACTCCCCGGC
1351 TCAGGCCAGGC CAGGATGGCG GGGTGGGTCC CTTTGCTGG GCTGGACTGT
1401 ACATATGTTA ATAGCGAAA CCCGACGCCA CATTGTTATA ATTGTGATT
1451 AACTTTATTG TACAAAAGTG TTGGTGGCGT GTATTTGGC AGGAGCGAGG
1501 GTTGGGGGT AGAGGGCACG GAGGGTTGTG CAAGTTGAAG AGAGGAAAA
1551 GTGGGTACCT GAAGTGTGGG GCAGGTAAAG GGGCCTTCAG GCAAGAGCCC
1601 AGACCTGCAAG AGACAGTCCG AGACTGTCTC GGACCCCCCTG ACAGGCTGCA
1651 GCAGCCGCAC CCGCACCGG AATACCCAC CAGTGGCCGC CAGGGTGGTG
1701 CCAAGGTCAG GCCTCCCTT CCTACAATCA CAGCTGCAGC TGGACCTCCG
1751 GCCTCCTGGG AAGCCCAGCA GGAGGGAAAG CCTGAGGTCA CACTGTGGG
1801 TGAGGTCAAC GCTGGCTCCA CCCACAGGCC CAGACCCCCCTT CAGCCCACTC
1851 TGCAAGTTCG AGCTTCATCC CCACCAAGTT CTCCGCTGGA CCCAGATGCC
1901 AGTGGAGCAC AGAGGCCCG CCAGGGGGCG CTTGGGGCA AGACTGGTGG
1951 GGGTTGTGGC TGGGCGGGTC TCTGTTCTG GAATGGGGCA GGAGGGAGAA
2001 CGAGGAGGCC CGCGAAGGAC GGTGTGCGGG CCGGCCAGGCC CTGGACGAAA
2051 GAAGAGGGCC CCTCCAGGCC AGTCTGGCA CCGTGGGATA GCGGCTGCAG
2101 GTAGGCAGAG GCGCTGCCAG TGCCCTAGGT GCCTTTCCT CCATCCGGCC
2151 CTTCCACCT TCCCTATAACC TTCCCTCCAC CTCCCTCAAC TCCGGCCTC
2201 CCCACCCCTT TACTGCTTC AAATCTCTT CCCTAAACCC TGACCCCTTC
2251 CTGCACCCCCA AGCCCGCCCC TCTCTCCGTA ACTCAGCCAT CAGCAGGGC
2301 AGACGGCAGG TGGCCTGGTT GCTGCAGCTC CCAGGATCAG CTCTGCCCTC
2351 CCGCCAAACG CCAGCCTCGT CACCGCTCCA GGGCACCTCC AGCACTAAC
2401 GGTGGTTGCA GCAGGTGGCA GCCAGCCCCCT GGATGAGCCA AGGTCTCTC
2451 CCCAGCCAGG CATGGCCGAC TCTGCACAGG CCCAGAAGCT GGTGTACCTG
2501 GTCACAGGGG GCTGTGGCTT CCTGGGAGAG CACGTGGTGC GAATGCTGCT
2551 GCAGCGGGAG CCCCGCTCG GGGAGCTGCG GGTCTTTGAC CAACACCTGG
2601 GTCCCTGGCT GGAGGAGCTG AAGACAGGTT CTTGTTGGGG GAGCTGTGG
2651 TGGAGAGGGT GTGGACGCTT CCCCCAACCT TCCCAAGCTG GGATCCCCAC
2701 CCCTGCAGTG GAACAGATGA TGCTGGTTTC TGTCACATG GATGGGTG
2751 GTGAGTCACA TTGGGAACGT GACTCCAGGG TGGAAAGATGA ACCCAGCCTC
2801 TGGCCTCTGG CCCCAGCTCT GACATGGCCT GTGTCCTCCA ACCCCGGCA
2851 GGGCCTGTGA GGGTGACTGC CATCCAGGGG GACGTGACCC AGGCCCCATGA
2901 GGTGGCAGCA GCTGTGGCCG GAGCCCATGT GGTCACTCCAC ACGGCTGGGC
2951 TGGTAGACGT GTTGGCAGG GCCAGTCCC AGACCATCCA TGAGGTCAAC
3001 GTGCAGGGTG AGGAGCTCTG GACACTCTG GCCATCTTC GCTGTTGTTC
3051 CCCACTCTGT CTTGGCCTT GACCTCCGGT GACTCCCCCTG GGACAAGTTG

FIGURE 3A

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3101 TCCTTATTGAC AGCCCTGCC 2500 CGGCCTCCCC TGACCTGTCA TGTTTTCTCC
3151 TGGACCTGGG ATGGGGAGGA GGAAGATGCA GAGAGGGAAG AAGCTGCAGC
3201 TTGGATACGC CTCCTCTCT GCAGGTACC CGAACGTGA TCGAGGCTTG
3251 TGTGCAGACC GGAACACGGT TCCGGTCTA CACCAGCAGC ATGGAAGTTG
3301 TGGGGCTAA CACCAAAGGT CACCCCTCT ACAGGTGAGT GGCAGGCCCT
3351 CTTGTCTCT AAGAGCCCAT TTCCCTCAGC ATTGAGTCTT CCTTCTCCTC
3401 CCACCAGGGG CAACGAAGAC ACCCCATACG AAGCAGTGCA CAGGCACCCC
3451 TATCCTTGCA GCAAGGCCCT GGCAGGTGG CTGGTCTTGG AGGCCAACGG
3501 GAGGAAGGT AGCCCAAGAA AAGGAGGCGC AGAGATGGGG CTCCCTGCCCT
3551 GCACACCCCC TTACCCCTGCC AGCCCAAGGA GGCCGGGCC GAGAGCAAGC
3601 TGTGGGTCTC CAGGTCTCAG CAGTACCTGC CTGGCACCAG AGGTCCTGG
3651 GGGGCTGCCCT CTGGTACGT GTGCCCTTCG TCCCACGGGC ATCTACGGTG
3701 AAGGCCACCA GATCATGAGG GACTTCTACC GCCAGGCCCT GCGCTGGGA
3751 GTTGGGTCTC TCCGGCCAT CCCGGCTCT GTGGAGCATG GCCGGGTCTA
3801 TGTGGGTGAG GACTGGCTA GGCAGGGGA GGCTGAGAAT ATGGCAGGAG
3851 GACTTGTCT AGAAGGGGGC AGGACCCACA TGGCCCTGGG AGAGAAGTGT
3901 GGACTCTGGC TAGAAAAATA TGGTCTATAC ATGGGCAAG GTAGACTGTG
3951 ATTATGTCTC CACAGCCTGC AGAGAATACA GGATCCATGC AAGTTGGGAC
4001 ATTAAAAAGT GTATCATAGG CTACAGAGAA GATTGCAAGT ATGGGAGCAG
4051 CCATCCCCCA GGAGAGGGAGA GGAGAGGGAC AGTGTCTACA CAGCACTAAA
4101 AGGGCTGGGT TCAGTGGCTC GCATCTATAA TCCCGACACT TTAGGAGGCT
4151 GAGGGGGAGA GATGGCTGA GCCAGGAGT TGGAGGCTGC AGTGAAGCTAT
4201 GACCGCACCA CTGCACTCCA GCCTGGATGA CAGAGACAGA CCCTGTCTCT
4251 AAAACTTTT TTAAAGGAAG TAGCATCTAC ACAGGAAATA AGGTCACCTG
4301 CCACTCCATC CTGCACTCCC CAAGCCTCTC AGGGCCACC ACGCAGGTCC
4351 TGGTTTCTCT ATCCTCTCCC CAGGTTCTT GCAGATGCA GCTGGCCAG
4401 GAGAGCAAGT GACTACCAGG GCGAGGGAGA AGGAGCCTT TCCCAGGCTG
4451 CTGTGGGGAT GTGGGCCGCA ACTACCTGGG CCGAAAGAGG GGGTGGCCCA
4501 GGAGAGCAGC CTCGATGTGG TGTGCAAGG GCACTCAGGG GTGTCGCCG
4551 CTCTCTTCCG CCACCGGCAG GCAATGTTGC CTGGATGCCAC GTGCTGGCAG
4601 CCCGGGAGCT GGAGCAGCGG GCAGCCCTGA TGGGCGGCCA GGTATACTTC
4651 TGCTACGATG GATCACCTCA CAGGAGCTAC GAGGATTCA ACATGGAGTT
4701 CCTGGGGCCC TGCGACTGC GGCTGGTGGG CGCCCGCCCA TTGCTGCCCT
4751 ACTGGCTGCT GGTGTTCTG GCTGCTCTCA ATGCCCTGCT GCAGTGGCTG
4801 CTGCGGCCAC TGGTGCCTCA CGCACCCCTG CTGAACCCCT ACACGCTGGC
4851 CGTGGCAAC ACCACCTCA CGTCAGCAC CGACAAGGCT CAGGCCATT
4901 TCGGCTATGA GCCCTGTTC TCGTGGGAGG ATAGCCGAC CCGCACCAATT
4951 CTCTGGGTAC AGGCCGCTAC GGGTTCAGCC CAGTGAAGGT GGGGCTGGGG
5001 CCTGGAGGCC CAGATACAGC ACATCCACCC AGGTCCCCAG CCCTCACACC
5051 CTGGACGGGA AGGGACAGCT GCATTCAGA GCGAGGAGCA GGGCTCTGG
5101 GCGCAGAATG GCTGCTCTTG TCGTAGAGCC CTCCACATTT TCTTTTCTT
5151 TTTTGAGACA GGGTCTGCT CTGTCACCCA GACTGGAGTG CAGTGGTGTG
5201 ATCATAGCTC ACTGCACCCCT CAACCTCTG GGTCAAGCA ATCCCTCTGC
5251 CTCAGCTCC TTGAACAGCT GGGACACAG GTGCACGCCA CCACACCTGG
5301 TTTTTTTTGT TTGTTTTTAG AGACAGGGTC TCACTATATT GCTCAGGCTG
5351 GCTTGAACCT CCTGGCTCA AGTGTCTTC CCACGTGGC CTCCAAAC
5401 GCTGGAACTA CAAAGTGTGAG CCACCGCGCC TGGCCCAAGC CCTCCACATT
5451 TCAATCCAG GAGCCTTGAG TCTGTGTTGT GTCCTGACAC CTCCAAGITC
5501 TAGGGCGTC AGGACACGGG AGGGTTTGGG GACAGAGTGT CCTTCTCTG
5551 TCCCTCATC CCAGCTCTGA TGGCCGTTG GTGAGTGTCT GGTGCCCTGG
5601 TGGCTGCCCT CAGCTCTCTT CTGGCTTCTC GAGCAGGAAG CGAGCAGAGG
5651 CTCCACAGGC TTACGCTGCT CTCCCTGACAG CCACACGCA CCCTCGGTGC
5701 AGAGTGCAGA GGCAGCTCTG GTTCCCTCCAG CCACCTCAGT CCCTTTTGG
5751 GAGGTGATGT TCCCATTGTT TTTCAAGGC CTCACCTTCA ACTGTCTGT
5801 TTAGAATTCC CCTCTGGAGG GCTATGGCTT CCCTATGCTT TCACTTCCCA
5851 CCTCTCTACC TAAGTTCTT CCCAGCACAT CGCCAGCCCT GGGCTGGGG
5901 ATGTCCCCAA TGCTGTACCT GGCTGACCCC GGATTAAG CCTCATCCAC
5951 GACCGTGTCC ATCTGTCTGT CCAGCTCTCC CTCCCATCCC CCCACCCCAT
6001 GTCCGCCTCC CCACGGCGCC CATCCACAGT GGGAGAGAAA GGAAGTGAGC
6051 ACACGGCACA CCCGCTGTTG GATTGGTTGC TATTTCTCCC GTCCACAGG
6101 GCCTGACCTG GCCCAGGGTG GGGTGGGGGG CTCTGGGAC AGGACATGCA
6151 GGGAGGAAGG GGGGGGCAGG ATTTCCTGT GTTTTATCCA TTTGCAAGTT

FIGURE 3B

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6201 GGTCAACCAAT AGAAATGGGA CTCTGAGGGC TAACAGAAAT GGGACTCTGA
 6251 GGGCTAACAG GAGAGGGCGG CCTGGCTCTG GGCCCCAGCC AGGCCCCAGG
 6301 AGTCCTGTCC CCTCTGAGAA GGGGAGGGAG AGAGCTCTAG AAACCAACGG
 6351 AGAAACAGAG AAGGGGGCAG GGGCTCATGT CAGCAAACAC GGCTACATCA
 6401 CGTGACACGC CAGTGACACA GAAACACAG CCAAACGCACA CGGCTGCACA
 6451 GCGGGCAGGG GCGGTTAGGG GAAAGGGAGC CGGGGCCACC CATTTGTCC
 6501 TCTGCAGGGC GGGCTGGGG GCAGGGTGAA TGCATAGAAC ACATCATGTG
 6551 TACACGCTCA GGGCGTGGCA AGAGCGTCCG TCGACCCACG GGTACATGGG
 6601 ATGGACACGC AGTGTGCTTC ATGAGGGGTG GGAACAGGGA GGAGGGGAA
 6651 GAGGAAGCAC TGAGCCCTGG CCAGGCCCCG GACCACCCGC AGGGCACACG
 6701 TGGGGCACAT GTGGGCTCAA TGGTTGCAGG CGCCTGGCA GGTAGCACAC
 6751 ATTTGTCCAA GAACATGCAA AAGACACAG CCTCCAGACA ACATGCCAGG
 6801 ACGCACACAG ACAGCAGCCA ACAAGCAGGC ACATCATAGG ATGTGGAGGA
 6851 CGCATAGAAA GGGCACAGCA GACCCTTAGA GATCCCCCTGG TCCACCTGAG
 6901 GCCCAGAGAT GGGCAGCTGT GGGCCAATG CCACTCCAGG TGGGGGAGT
 6951 GGTCCCCAG CCACGCTTCA ACCCTTCTCC TGTGGCCCA AGGCCGTGGG
 7001 ACTTCCGGAA ACACCTGGC TGAATGGGG TCCCTGTCCAG GCGGGCGGAA
 7051 GAGGGGACTG GGGGCTGGGG CCTGCTCTGA TGTCTCCCA GCAGGGCGAG
 7101 ATGGGAGCAG GAGGGCCGTG GCCAGACTTG GGGCAGACTT CCTGCTCTGC
 7151 AGAGGGGCGT TCTGGGAAGG GACAGGCAGG CCCCCAGCTC AGGACAGCCC
 7201 ACCTGGGGTT ACGCACGTGG CCACACTGAC ACACACACAG GACAAGGGAG
 7251 AGCTCGGCTG TCTGAGCTCG GGTAGAGGTG GAGGGGTACT GTGTTCTGGG
 7301 A

(SEQ ID NO: 3)

FEATURES:

Start: 2462
 Exon: 2462-2627
 Intron: 2628-3225
 Exon: 3226-3334
 Intron: 3335-3407
 Exon: 3408-3507
 Intron: 3508-3642
 Exon: 3643-3805
 Intron: 3806-4570
 Exon: 4571-4983
 Stop: 4984

SNPs:

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
1010	A	G	Beyond ORF(5')			
1151	C	T	Beyond ORF(5')			
4805	G	A	Exon	258	R	Q
6293	G	A	Beyond ORF(3')			

Context:

DNA Position

1010 TCCAAGCAGCCCATTGGCGTGGACGAGGAGATCACCTACGACTACAAGTCCCCACTGGAA
 GACAACAAGATCCCGTGTCTGTGTGGCACAGAGAGCTGCCGGGGCTCCCTAACTGAGGT
 GGGGCAAGGATGGGTGCCACACCCCTATTATTCCCCCTGGTGCCCTGAGCTCCCAGCAC
 CCCCCCAGCTTAGTGGGCTCAGCAGGGCCCACATGGCCCCATCTCAAGCGTGGGGTTG
 GGGGCCCCAAGCCCAGCGAGGGAGCCTCAGTCCCTGGAGGCAGCTCTGCCTCTCCTGTC
 [A;G]
 CCCCTGCCACCAACCCCTGATTGTTTCTTGTGGAGAAGAAGCTGTAAATGTTTGT
 AGCAGCCAGCAGCTGTGTTCTGTGAAACCTGGGTGCCGCTGTACAGATTCTGTCT

FIGURE 3C

Docket No. CL001181DIV2
Serial No. To Be Assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEINS...

GGGGGGCTACACAGTCTCTCGCTTGTGTTAATGGGGACTTCCCTTACGCCCTGCGTG
TACCCCTCCCCAGTTAGGGGCTCTGGGGCAGTGGCCATGTTCTCCCTGGGGGGCT
CTGCACCCCCAGTCTGGGACTCCGTGCGCTGGAACCCCTGCCATCTGTTCTGCCAGA

1151 CCCCTATTTATCCTGGTGCCTGAGCTCCAGCACCCCCCAGCCTAGTGGGCTC
AGCAGGGCCCACATGCCCATCTCAAGCGTGGGGTGGGGGCCAACGCCAGCGAGG
GAGCCTCAGTCCCTGGAGGGAGCTTCTGCTCTGCCCCCTGCCAACACCCTG
ATTGTTTTCTTGCAGAGAAGCTGAAATGTTGTAGCAGCCAGCAGCTGTTCC
TGTGGAAACCTGGGTGCCGGCTGTACAGATTCTGCTCTGGGGCTACACAGTCCCT
[C, T]

GCTTTGTGTTAATGGGACTTCCCTTACGCCCTGCGTGACCCCTCCCCAGTTAGGGG
TCTCTGGGAGTGGCCATGTTCTCCCTGGGGGCTCTGACCCCCAGTCTGGGG
CTCCGTGCCCTGGAACCCCTGCCATCTGTTCTGCCAGACCCCTGAGGGTCAACCTTAC
CCTGGTGTCACTCCCCGGCTAGCCAGGCCAGGATGGCGGGTGGTCCCTTGCTGG
CTGGACTGTACATATGTTAATAGCGAAACCCGACGCCACATTATAATTGTGATTA

4805 AGCAGCCCTCGATGTGGTGTGCAAGGGCACTCAGGGTGTGTCGCCCTCTTCCCGCCAC
CGGCAGGCAATGTTGCCCTGGATGCACTGCTGGCAGCCGGAGCTGGAGCAGCGGGCAG
CCCTGATGGCGGCCAGGTATACCTCTGCTACGATGGATCACCTACAGGAGCTACGAGG
ATTCAACATGGAGTTCCCTGGGCCCCTGCCAGTGGCGCTGGTGGCGCCGCCATTGC
TGCCCTACTGGCTGCTGGTGTCCCTGGCTGCCCTCAATGCCCTGCGTAGTGGCTGCT
[G, A]
GCCACTGGTGTCTACGCACCCCTGCTGAACCCCTACACGCTGGCGTGGCAAACACCAC
CTTCACCGTCAGCACCGACAAGGCTCAGGCCATTCCGCTATGAGCCCTGTTCTG
GGAGGATAGCGGACCCGACCATCTGGGTACAGGCCCTACGGGTTACGCCAGTG
ACGGTGGGCTGGGCTGGAGGGCCAGATACAGCACATCCACCCAGGTCCCAGCCCTC
ACACCCCTGGACGGGAAGGGACAGCTGCAATTCCAGAGCAGGAGGAGGCTTCTGGGCCA

6293 CACCCCATGTCCGCCCTCCCCACGGCGCCATCCACGTGGGACAGAAGGAAGTGGAC
ACGGCACACCCGCTGGATGGTGTGTTCTCCCTGGGACAGGACATGCACTGAGCAG
CCAGGGTGGGGTGGGGGCTCTGGGACAGGACATGCACTGAGGAGGAAGGGGGGGCAGGAT
TTTCTGTGTTTATCCATTGCAAGTTGGTCACCAATAGAAATGGACTCTGAGGGCTA
ACAGAAATGGGACTCTGAGGGCTAACAGGAGAGGGCCCTGGCTCTGGGCCAGCCAG
[G, A]
CCCCAGGAGTCTGCTCCCTCTGAGAAGGGAGGGAGAGCTCTAGAAACCAACGGAGA
AACAGAGAAGGGGGCAGGGCTCATGTCAGCAAACACGGCTACATCAGTGACACGCCAG
TGACACAGAAACACGCCAACGGCACACGGCTGCACAGCGGGCAGGGCGGTAGGGGAA
AGGGAGGCCGGGCCACCCATCTGCTCTGCAAGGGGGCTGGGGCAGGGTGAATGC
ATAGAACACATCATGTTACACGCTCAGGGCTGGCAAGAGCGTGCACCCACGGG

Chromosome map:
Chromosome 12

FIGURE 3D